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Sequence Listing could not be accepted.

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Reviewer: markspencer

Timestamp: [year=2008; month=12; day=2; hr=15; min=14; sec=30; ms=124;]

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Reviewer Comments:

<210> 9

<211> 527

<212> PRT

<213> protein p12 of T2 phage

* * * * *

<210> 10

<211> 527

<212> PRT

<213> protein p12 of T4 phage

* * * * *

<210> 11

<211> 518

<212> PRT

<213> protein p12 of PP01 phage

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<210> 12

<211> 516

<212> PRT

<213> protein p12 of RB69 phage

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<210> 13

<211> 516

<212> PRT

<213> protein p12 of AR1 phage

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<210> 14

<211> 527

<212> PRT

<213> protein p12 of K3 phage

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<210> 15
<211> 516
<212> PRT
<213> protein p12 of RB32-33 phage
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For SEQ ID # 9 through 15, numeric identifier <213> can only be one of three choices, "Scientific name, i.e. Genus/species, Unknown or Artificial Sequence." Please move any information that is not part of the "Genus/species" into a feature.

Application No: 10583415 Version No: 1.0

Input Set:

Output Set:

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Finished: 2008-10-31 10:24:01.953
Elapsed: 0 hr(s) 0 min(s) 1 sec(s) 535 ms
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Total Errors: 0
No. of SeqIDs Defined: 15
Actual SeqID Count: 15

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<110> MEYER, ROMAN
 SCHUTZ, MICHAEL
 GRALLERT, HOLGER
 GRASSL, RENATE
 MILLER, STEFAN

<120> ENDOTOXIN DETECTION METHOD

<130> DEBE:067US

<140> 10583415

<141> 2008-10-31

<150> PCT/DE2004/002778

<151> 2004-12-20

<150> DE 103 60 844.3

<151> 2003-12-20

<160> 15

<170> PatentIn version 3.3

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aatacatatc aacacggt 78

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<212> DNA

<213> artificial sequence

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<223> Synthetic primer

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<213> artificial sequence

<220>

<223> Synthetic primer

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gaaggaacta gtcatatggc ttgttggagc caccgcagc tcgaaaaagg cgccagtaat 60

aatacatatc aacacggt 78

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<211> 78

<212> DNA

<213> artificial sequence

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<223> Synthetic primer

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aatacatatc aacacggt 78

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<213> artificial sequence

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<223> strep tag

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Thr Tyr Gln

<210> 6

<211> 19

<212> PRT

<213> artificial sequence

<220>

<223> strep tag

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Met Ala Cys Trp Ser His Pro Gln Phe Glu Lys Gly Ala Ser Asn Asn

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Thr Tyr Gln

<210> 7
<211> 19
<212> PRT
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Met Ala Ser Trp Ser His Pro Gln Phe Glu Lys Gly Ala Cys Asn Asn
1 5 10 15

Thr Tyr Gln

<210> 8
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<212> PRT
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Thr Tyr Gln His Val Ser Asn Glu Ser Arg Tyr Val Lys Phe Asp Pro
20 25 30

Thr Asp Thr Asn Phe Pro Pro Glu Ile Thr Asp Val Gln Ala Ala Ile
35 40 45

Ala Ala Ile Ser Pro Ala Gly Val Asn Gly Val Pro Asp Ala Ser Ser
50 55 60

Thr Thr Lys Gly Ile Leu Phe Leu Ala Thr Glu Gln Glu Val Ile Asp
65 70 75 80

Gly Thr Asn Asn Thr Lys Ala Val Thr Pro Ala Thr Leu Ala Thr Arg
85 90 95

Leu Ser Tyr Pro Asn Ala Thr Glu Ala Val Tyr Gly Leu Thr Arg Tyr
100 105 110

Ser Thr Asp Asp Glu Ala Ile Ala Gly Val Asn Asn Glu Ser Ser Ile		
115	120	125
Thr Pro Ala Lys Phe Thr Val Ala Leu Asn Asn Val Phe Glu Thr Arg		
130	135	140
Val Ser Thr Glu Ser Ser Asn Gly Val Ile Lys Ile Ser Ser Leu Pro		
145	150	155 160
Gln Ala Leu Ala Gly Ala Asp Asp Thr Thr Ala Met Thr Pro Leu Lys		
165	170	175
Thr Gln Gln Leu Ala Val Lys Leu Ile Ala Gln Ile Ala Pro Ser Lys		
180	185	190
Asn Ala Ala Thr Glu Ser Glu Gln Gly Val Ile Gln Leu Ala Thr Val		
195	200	205
Ala Gln Ala Arg Gln Gly Thr Leu Arg Glu Gly Tyr Ala Ile Ser Pro		
210	215	220
Tyr Thr Phe Met Asn Ser Thr Ala Thr Glu Glu Tyr Lys Gly Val Ile		
225	230	235 240
Lys Leu Gly Thr Gln Ser Glu Val Asn Ser Asn Asn Ala Ser Val Ala		
245	250	255
Val Thr Gly Ala Thr Leu Asn Gly Arg Gly Ser Thr Thr Ser Met Arg		
260	265	270
Gly Val Val Lys Leu Thr Thr Thr Ala Gly Ser Gln Ser Gly Gly Asp		
275	280	285
Ala Ser Ser Ala Leu Ala Trp Asn Ala Asp Val Ile His Gln Arg Gly		
290	295	300
Gly Gln Thr Ile Asn Gly Thr Leu Arg Ile Asn Asn Thr Leu Thr Ile		
305	310	315 320
Ala Ser Gly Gly Ala Asn Ile Thr Gly Thr Val Asn Met Thr Gly Gly		
325	330	335

Tyr Ile Gln Gly Lys Arg Val Val Thr Gln Asn Glu Ile Asp Arg Thr
340 345 350

Ile Pro Val Gly Ala Ile Met Met Trp Ala Ala Asp Ser Leu Pro Ser
355 360 365

Asp Ala Trp Arg Phe Cys His Gly Gly Thr Val Ser Ala Ser Asp Cys
370 375 380

Pro Leu Tyr Ala Ser Arg Ile Gly Thr Arg Tyr Gly Gly Ser Ser Ser
385 390 395 400

Asn Pro Gly Leu Pro Asp Met Arg Gly Leu Phe Val Arg Gly Ser Gly
405 410 415

Arg Gly Ser His Leu Thr Asn Pro Asn Val Asn Gly Asn Asp Gln Phe
420 425 430

Gly Lys Pro Arg Leu Gly Val Gly Cys Thr Gly Gly Tyr Val Gly Glu
435 440 445

Val Gln Lys Gln Gln Met Ser Tyr His Lys His Ala Gly Gly Phe Gly
450 455 460

Glu Tyr Asp Asp Ser Gly Ala Phe Gly Asn Thr Arg Arg Ser Asn Phe
465 470 475 480

Val Gly Thr Arg Lys Gly Leu Asp Trp Asp Asn Arg Ser Tyr Phe Thr
485 490 495

Asn Asp Gly Tyr Glu Ile Asp Pro Ala Ser Gln Arg Asn Ser Arg Tyr
500 505 510

Thr Leu Asn Arg Pro Glu Leu Ile Gly Asn Glu Thr Arg Pro Trp Asn
515 520 525

Ile Ser Leu Asn Tyr Ile Ile Lys Val Lys Glu
530 535

<210> 9

<211> 527

<212> PRT

<213> protein p12 of T2 phage

<400> 9

Met Ser Asn Asn Thr Tyr Gln His Val Ser Asn Glu Ser Arg Tyr Val
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Lys Phe Asp Pro Thr Asp Thr Asn Phe Pro Pro Glu Ile Thr Asp Val
20 25 30

Gln Ala Ala Ile Ala Ala Ile Ser Pro Ala Gly Val Asn Gly Val Pro
35 40 45

Asp Ala Ser Ser Thr Thr Lys Gly Ile Leu Phe Leu Ala Thr Glu Gln
50 55 60

Glu Val Ile Asp Gly Thr Asn Asn Thr Lys Ala Val Thr Pro Ala Thr
65 70 75 80

Leu Ala Thr Arg Leu Ser Tyr Pro Asn Ala Thr Glu Ala Val Tyr Gly
85 90 95

Leu Thr Arg Tyr Ser Thr Asp Asp Glu Ala Ile Ala Gly Val Asn Asn
100 105 110

Glu Ser Ser Ile Thr Pro Ala Lys Phe Thr Val Ala Leu Asn Asn Val
115 120 125

Phe Glu Thr Arg Val Ser Thr Glu Ser Ser Asn Gly Val Ile Lys Ile
130 135 140

Ser Ser Leu Pro Gln Ala Leu Ala Gly Ala Asp Asp Thr Thr Ala Met
145 150 155 160

Thr Pro Leu Lys Thr Gln Gln Leu Ala Val Lys Leu Ile Ala Gln Ile
165 170 175

Ala Pro Ser Lys Asn Ala Ala Thr Glu Ser Glu Gln Gly Val Ile Gln
180 185 190

Leu Ala Thr Val Ala Gln Ala Arg Gln Gly Thr Leu Arg Glu Gly Tyr
195 200 205

Ala Ile Ser Pro Tyr Thr Phe Met Asn Ser Thr Ala Thr Glu Glu Tyr
210 215 220

Lys Gly Val Ile Lys Leu Gly Thr Gln Ser Glu Val Asn Ser Asn Asn
 225 230 235 240

Ala Ser Val Ala Val Thr Gly Ala Thr Leu Asn Gly Arg Gly Ser Thr
 245 250 255

Thr Ser Met Arg Gly Val Val Lys Leu Thr Thr Thr Ala Gly Ser Gln
 260 265 270

Ser Gly Gly Asp Ala Ser Ser Ala Leu Ala Trp Asn Ala Asp Val Ile
 275 280 285

His Gln Arg Gly Gly Gln Thr Ile Asn Gly Thr Leu Arg Ile Asn Asn
 290 295 300

Thr Leu Thr Ile Ala Ser Gly Gly Ala Asn Ile Thr Gly Thr Val Asn
 305 310 315 320

Met Thr Gly Gly Tyr Ile Gln Gly Lys Arg Val Val Thr Gln Asn Glu
 325 330 335

Ile Asp Arg Thr Ile Pro Val Gly Ala Ile Met Met Trp Ala Ala Asp
 340 345 350

Ser Leu Pro Ser Asp Ala Trp Arg Phe Cys His Gly Gly Thr Val Ser
 355 360 365

Ala Ser Asp Cys Pro Leu Tyr Ala Ser Arg Ile Gly Thr Arg Tyr Gly
 370 375 380

Gly Thr Ser Ser Asn Pro Gly Leu Pro Asp Met Arg Gly Leu Phe Val
 385 390 395 400

Arg Gly Ser Gly Arg Gly Ser His Leu Thr Asn Pro Asn Val Asn Gly
 405 410 415

Asn Asp Gln Phe Gly Lys Pro Arg Leu Gly Val Gly Cys Thr Gly Gly
 420 425 430

Tyr Val Gly Glu Val Gln Lys Gln Gln Met Ser Tyr His Lys His Ala
 435 440 445

Gly Gly Phe Gly Glu Tyr Asp Asp Ser Gly Ala Phe Gly Asn Thr Arg
450 455 460

Arg Ser Asn Phe Val Gly Thr Arg Lys Gly Leu Asp Trp Asp Asn Arg
465 470 475 480

Ser Tyr Phe Thr Asn Asp Gly Tyr Glu Ile Asp Pro Ala Ser Gln Arg
485 490 495

Asn Ser Arg Tyr Thr Leu Asn Arg Pro Glu Leu Ile Gly Asn Glu Thr
500 505 510

Arg Pro Trp Asn Ile Ser Leu Asn Tyr Ile Ile Lys Val Lys Glu
515 520 525

<210> 10

<211> 527

<212> PRT

<213> protein p12 of T4 phage

<400> 10

Met Ser Asn Asn Thr Tyr Gln His Val Ser Asn Glu Ser Arg Tyr Val
1 5 10 15

Lys Phe Asp Pro Thr Asp Thr Asn Phe Pro Pro Glu Ile Thr Asp Val
20 25 30

His Ala Ala Ile Ala Ala Ile Ser Pro Ala Gly Val Asn Gly Val Pro
35 40 45

Asp Ala Ser Ser Thr Thr Lys Gly Ile Leu Phe Ile Pro Thr Glu Gln
50 55 60

Glu Val Ile Asp Gly Thr Asn Asn Thr Lys Ala Val Thr Pro Ala Thr
65 70 75 80

Leu Ala Thr Arg Leu Ser Tyr Pro Asn Ala Thr Glu Thr Val Tyr Gly
85 90 95

Leu Thr Arg Tyr Ser Thr Asn Asp Glu Ala Ile Ala Gly Val Asn Asn
100 105 110

Glu Ser Ser Ile Thr Pro Ala Lys Phe Thr Val Ala Leu Asn Asn Ala
115 120 125

Phe Glu Thr Arg Val Ser Thr Glu Ser Ser Asn Gly Val Ile Lys Ile
130 135 140

Ser Ser Leu Pro Gln Ala Leu Ala Gly Ala Asp Asp Thr Thr Ala Met
145 150 155 160

Thr Pro Leu Lys Thr Gln Gln Leu Ala Ile Lys Leu Ile Ala Gln Ile
165 170 175

Ala Pro Ser Glu Thr Thr Ala Thr Glu Ser Asp Gln Gly Val Val Gln
180 185 190

Leu Ala Thr Val Ala Gln Val Arg Gln Gly Thr Leu Arg Glu Gly Tyr
195 200 205

Ala Ile Ser Pro Tyr Thr Phe Met Asn Ser Ser Ser Thr Glu Glu Tyr
210 215 220

Lys Gly Val Ile Lys Leu Gly Thr Gln Ser Glu Val Asn Ser Asn Asn
225 230 235 240

Ala Ser Val Ala Val Thr Gly Ala Thr Leu Asn Gly Arg Gly Ser Thr
245 250 255

Thr Ser Met Arg Gly Val Val Lys Leu Thr Thr Thr Ala Gly Ser Gln
260 265 270

Ser Gly Gly Asp Ala Ser Ser Ala Leu Ala Trp Asn Ala Asp Val Ile
275 280 285

Gln Gln Arg Gly Gly Gln Ile Ile Tyr Gly Thr Leu Arg Ile Glu Asp
290 295 300

Thr Phe Thr Ile Ala Asn Gly Gly Ala Asn Ile Thr Gly Thr Val Arg
305 310 315 320

Met Thr Gly Gly Tyr Ile Gln Gly Asn Arg Ile Val Thr Gln Asn Glu
325 330 335

Ile Asp Arg Thr Ile Pro Val Gly Ala Ile Met Met Trp Ala Ala Asp
340 345 350

Ser Leu Pro Ser Asp Ala Trp Arg Phe Cys His Gly Gly Thr Val Ser
355 360 365

Ala Ser Asp Cys Pro Leu Tyr Ala Ser Arg Ile Gly Thr Arg Tyr Gly
370 375 380

Gly Asn Pro Ser Asn Pro Gly Leu Pro Asp Met Arg Gly Leu Phe Val
385 390 395 400

Arg Gly Ser Gly Arg Gly Ser His Leu Thr Asn Pro Asn Val Asn Gly
405 410 415

Asn Asp Gln Phe Gly Lys Pro Arg Leu Gly Val Gly Cys Thr Gly Gly
420 425 430

Tyr Val Gly Glu Val Gln Ile Gln Gln Met Ser Tyr His Lys His Ala
435 440 445

Gly Gly Phe Gly Glu His Asp Asp Leu Gly Ala Phe Gly Asn Thr Arg
450 455 460

Arg Ser Asn Phe Val Gly Thr Arg Lys Gly Leu Asp Trp Asp Asn Arg
465 470 475 480

Ser Tyr Phe Thr Asn Asp Gly Tyr Glu Ile Asp Pro Glu Ser Gln Arg
485 490 495

Asn Ser Lys Tyr Thr Leu Asn Arg Pro Glu Leu Ile Gly Asn Glu Thr
500 505 510

Arg Pro Trp Asn Ile Ser Leu Asn Tyr Ile Ile Lys Val Lys Glu
515 520 525

<210> 11
<211> 518
<212> PRT
<213> protein p12 of PP01 phage

<400> 11

Met Ser Asn Asn Thr Tyr Gln His Val Ser Asn Glu Ser Lys Tyr Val
1 5 10 15

Lys Phe Asp Pro Val Gly Ser Asn Phe Pro Asp Thr Val Thr Thr Val

20

25

30

Gln Ser Ala Leu Ser Lys Ile Ser Asn Ile Gly Val Asn Gly Ile Pro
 35 40 45

Asp Ala Ser Met Glu Val Lys Gly Ile Ala Met Ile Ala Ser Glu Gln
 50 55 60

Glu Val Leu Asp Gly Thr Asn Asn Ser Lys Ile Val Thr Pro Ala Thr
 65 70 75 80

Leu Ala Thr Arg Leu Leu Tyr Pro Asn Ala Thr Glu Thr Lys Tyr Gly
 85 90 95

Leu Thr Arg Tyr Ser Thr Asn Glu Glu Thr Leu Glu Gly Ser Asp Asn
 100 105 110

Asn Ser Ser Ile Thr Pro Gln Lys Leu Lys Tyr His Thr Asp Asp Val
 115 120 125

Phe Gln Asn Arg Tyr Ser Ser Glu Ser Ser Asn Gly Val Ile Lys Ile
 130 135 140

Ser Ser Thr Pro Ala Ala Leu Ala Gly Val Asp Asp Thr Thr Ala Met
 145 150 155 160

Thr Pro Leu Lys Thr Gln Lys Leu Ala Ile Lys Leu Ile Ser Gln Ile
 165 170 175

Ala Pro Ser Glu Asp Thr Ala Ser Glu Ser Val Arg Gly Val Val Gln
 180 185 190

Leu Ser Thr Val Ala Gln Thr Arg Gln Gly Thr Leu Arg Glu Gly Tyr
 195